

1
SEQUENCE LISTING

<110> PAKOLA, STEVE
DE SMET, MARK

<120> PHARMACOLOGICAL VITREOLYSIS

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<140> 10/729,475
<141> 2003-12-05

<150> GB 0228409.9
<151> 2002-12-06

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<170> PatentIn Ver. 3.2

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Primer

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<211> 750
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(747)

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cct gga agg gtt gtg ggg ggg tgg tgg	gtg	gcc	cac	cca	cat	tcc	tgg	ccc	96								
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tgg	caa	gtc	agt	ctt	aga	aca	agg	ttt	gga	atg	cac	ttc	tgt	gga	ggc	144	
Trp	Gln	Val	Ser	Leu	Arg	Thr	Arg										
35								40					45				
acc	ttg	ata	tcc	cca	gag	tgg	gtg	ttg	act	gct	gcc	cac	tgc	ttg	gag	192	
Thr	Leu	Ile	Ser	Pro	Glu	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Leu	Glu		
50								55			60						
aag	tcc	cca	agg	cct	tca	tcc	tac	aag	gtc	atc	ctg	ggt	gca	cac	caa	240	
Lys	Ser	Pro	Arg	Pro	Ser	Ser	Tyr	Lys	Val	Ile	Leu	Gly	Ala	His	Gln		
65								70			75			80			
gaa	gtg	aat	ctc	gaa	ccg	cat	gtt	cag	gaa	ata	gaa	gtg	tct	agg	ctg	288	
Glu	Val	Asn	Leu	Glu	Pro	His	Val	Gln	Glu	Ile	Glu	Val	Ser	Arg	Leu		
85								90					95				
ttc	ttg	gag	ccc	aca	cga	aaa	gat	att	gcc	ttg	cta	aag	cta	agc	agt	336	
Phe	Leu	Glu	Pro	Thr	Arg	Lys	Asp		Ile	Ala	Leu	Leu	Lys	Leu	Ser	Ser	
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cct	gcc	gtc	atc	act	gac	aaa	gta	atc	cca	gct	tgt	ctg	cca	tcc	cca	384	
Pro	Ala	Val	Ile	Thr	Asp	Lys	Val	Ile	Pro	Ala	Cys	Leu	Pro	Ser	Pro		
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Asn	Tyr	Val	Val	Ala	Asp	Arg	Thr	Glu	Cys	Phe	Ile	Thr	Gly	Trp	Gly		
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Glu	Thr	Gln	Gly	Thr	Phe	Gly	Ala	Gly	Leu	Leu	Lys	Glu	Ala	Gln	Leu		
145								150			155			160			
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Pro	Val	Ile	Glu	Asn	Lys	Val	Cys	Asn	Arg	Tyr	Glu	Phe	Leu	Asn	Gly		
165								170			175						
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Arg	Val	Gln	Ser	Thr	Glu	Leu	Cys	Ala	Gly	His	Leu	Ala	Gly	Gly	Thr		
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Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Phe	Glu	Lys		
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gac	aaa	tac	att	tta	caa	gga	gtc	act	tct	tgg	ggt	ctt	ggc	tgt	gca	672	
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Arg	Pro	Asn	Lys	Pro	Gly	Val	Tyr	Val	Arg	Val	Ser	Arg	Phe	Val	Thr		
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Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu			
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Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln			
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Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu			
85	90	95	
Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser			
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Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro			
115	120	125	
Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly			
130	135	140	
Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu			
145	150	155	160
Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly			
165	170	175	
Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr			
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Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys			
195	200	205	
Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala			
210	215	220	
Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr			
225	230	235	240
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<211> 27
<212> DNA
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<220>
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<212> DNA
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                                         10

gaa gac tgt atg ttt ggg aat ggg aaa gga tac cga ggc aag agg gcg      96
Glu Asp Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala
      20           25           30
                                         30

acc act gtt act ggg acg cca tgc cag gac tgg gct gcc cag gag ccc      144
Thr Thr Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro
      35           40           45
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cat aga cac agc att ttc act cca gag aca aat cca cgg gcg ggt ctg      192
His Arg His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu
      50           55           60
                                         60

gaa aaa aat tac tgc cgt aac cct gat ggt gat gta ggt ggt ccc tgg      240
Glu Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp
      65           70           75           80
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85 90 95	
cag tgt gcg gcc cct tca ttt gat tgt ggg aag cct caa gtg gag ccg	336
Gln Cys Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro	
100 105 110	
aag aaa tgt cct gga agg gtt gtg ggg ggg tgt gtg gcc cac cca cat	384
Lys Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His	
115 120 125	
tcc tgg ccc tgg caa gtc agt ctt aga aca agg ttt gga atg cac ttc	432
Ser Trp Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe	
130 135 140	
tgt gga ggc acc ttg ata tcc cca gag tgg gtg ttg act gct gcc cac	480
Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His	
145 150 155 160	
tgc ttg gag aag tcc cca agg cct tca tcc tac aag gtc atc ctg ggt	528
Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly	
165 170 175	
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Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val	
180 185 190	
tct agg ctg ttc ttg gag ccc aca cga aaa gat att gcc ttg cta aag	624
Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys	
195 200 205	
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Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu	
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225 230 235 240	
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290 295 300	

ttc gag aag gac aaa tac att tta caa gga gtc act tct tgg ggt ctt	960
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Glu Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp	
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85 90 95	
Gln Cys Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro	
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Lys Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His	
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165 170 175	
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180 185 190	
Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys	
195 200 205	

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 Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr
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 Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe
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 275 280 285
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 290 295 300
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<220>
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 <222> (1)...(2373)

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 Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg Lys Ser Ser
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 65 70 75 80

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Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr Met			
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tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt tcc act tct	336		
Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser Thr Ser			
100	105	110	
ccc cac aga cct aga ttc tca cct gct aca cac ccc tca gag gga ctg	384		
Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu Gly Leu			
115	120	125	
gag gag aac tac tgc agg aat cca gac aac gat ccg cag ggg ccc tgg	432		
Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly Pro Trp			
130	135	140	
tgc tat act act gat cca gaa aag aga tat gac tac tgc gac att ctt	480		
Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp Ile Leu			
145	150	155	160
gag tgt gaa gag gaa tgt atg cat tgc agt gga gaa aac tat gac ggc	528		
Glu Cys Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr Asp Gly			
165	170	175	
aaa att tcc aag acc atg tct gga ctg gaa tgc cag gcc tgg gac tct	576		
Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp Asp Ser			
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cag agc cca cac gct cat gga tac att cct tcc aaa ttt cca aac aag	624		
Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys			
195	200	205	
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Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu Arg Pro			
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Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys Asp Ile			
225	230	235	240
ccc cgc tgc aca aca cct cca cca tct tct ggt ccc acc tac cag tgt	768		
Pro Arg Cys Thr Thr Pro Pro Ser Ser Gly Pro Thr Tyr Gln Cys			
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ctg aag gga aca ggt gaa aac tat cgc ggg aat gtg gct gtt acc gtt	816		
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Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp Ser Ser	
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Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val	
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675 680 685	
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Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser	
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Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys	
740 745 750	

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Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile	
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780	
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Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp Ile Leu	
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155	160
Glu Cys Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr Asp Gly	
165	170
175	
Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp Asp Ser	
180	185
190	
Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys	
195	200
205	

Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu Arg Pro
 210 215 220
 Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys Asp Ile
 225 230 235 240
 Pro Arg Cys Thr Thr Pro Pro Ser Ser Gly Pro Thr Tyr Gln Cys
 245 250 255
 Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val Thr Val
 260 265 270
 Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His Thr His
 275 280 285
 Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu Asn Tyr
 290 295 300
 Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr Thr Asn
 305 310 315 320
 Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp Ser Ser
 325 330 335
 Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro Glu Leu Thr
 340 345 350
 Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr Arg Gly
 355 360 365
 Thr Ser Ser Thr Thr Thr Gly Lys Lys Cys Gln Ser Trp Ser Ser
 370 375 380
 Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr Pro Asn Ala
 385 390 395 400
 Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp Lys Gly Pro
 405 410 415
 Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr Cys Asn Leu
 420 425 430
 Lys Lys Cys Ser Gly Thr Glu Ala Ser Val Val Ala Pro Pro Pro Val
 435 440 445
 Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu Glu Asp Cys Met Phe
 450 455 460
 Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala Thr Thr Val Thr Gly
 465 470 475 480
 Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro His Arg His Ser Ile
 485 490 495
 Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys Asn Tyr Cys
 500 505 510

Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr Thr Thr Asn
 515 520 525

Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro Gln Cys Ala Ala Pro
 530 535 540

Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys Cys Pro Gly
 545 550 555 560

Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro Trp Gln
 565 570 575

Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly Thr Leu
 580 585 590

Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser
 595 600 605

Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val
 610 615 620

Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu
 625 630 635 640

Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala
 645 650 655

Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr
 660 665 670

Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr
 675 680 685

Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val
 690 695 700

Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val
 705 710 715 720

Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser
 725 730 735

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys
 740 745 750

Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro
 755 760 765

Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile
 770 775 780

Glu Gly Val Met Arg Asn Asn
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